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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=3; day=13; hr=11; min=48; sec=9; ms=975;]

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Application No: 10593071 Version No: 2.0

Input Set:

Output Set:

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Finished: 2008-02-29 14:58:54.041
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 523 ms
Total Warnings: 2
Total Errors: 0
No. of SeqIDs Defined: 15
Actual SeqID Count: 15

Error code	Error Description
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SEQUENCE LISTING

<110> ROUGEOT, Catherine
HUAULME, Jean-Francois
UNGEHEUER, Marie-Noelle
WISNER, Anne
DUFOUR, Evelyne

<120> PEPTIDES DERIVED FROM HUMAN BPLP PROTEIN, POLYNUCLEOTIDES CODING
FOR SAID PEPTIDES AND ANTIBODIES DIRECTED AGAINST SAID PEPTIDES

<130> 296415US0PCT

<140> 10593071

<141> 2008-02-29

<150> PCT/IB05/00700

<151> 2005-03-18

<150> EPO 04290754.3

<151> 2004-03-19

<160> 15

<170> PatentIn version 3.3

<210> 1

<211> 947

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81)..(686)

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ccaaggagca acttttaaaga atg aaa tta act ttc ttc ttg ggc ctg ttg gct 113

Met Lys Leu Thr Phe Phe Leu Gly Leu Leu Ala

1 5 10

ctt att tca tgt ttc aca ccc agt gag agt caa aga ttc tcc aga aga 161

Leu Ile Ser Cys Phe Thr Pro Ser Glu Ser Gln Arg Phe Ser Arg Arg

15 20 25

cca tat cta cct ggc cag ctg cca cca cct cca ctc tac agg cca aga 209

Pro Tyr Leu Pro Gly Gln Leu Pro Pro Pro Pro Leu Tyr Arg Pro Arg

30 35 40

tgg gtt cca cca agt ccc cca cct ccc tat gac tca aga ctt aat tca 257

Trp Val Pro Pro Ser Pro Pro Pro Pro Tyr Asp Ser Arg Leu Asn Ser

45 50 55

cca ctt tct ctt ccc ttt gtc cca ggg cga gtt cca cca tct tct ttc 305

Pro Leu Ser Leu Pro Phe Val Pro Gly Arg Val Pro Pro Ser Ser Phe
60 65 70 75

tct cga ttt agc caa gca gtc att cta tct caa ctc ttt cca ttg gaa 353
Ser Arg Phe Ser Gln Ala Val Ile Leu Ser Gln Leu Phe Pro Leu Glu
80 85 90

tct att aga caa cct cga ctc ttt ccg ggt tat cca aac cta cat ttc 401
Ser Ile Arg Gln Pro Arg Leu Phe Pro Gly Tyr Pro Asn Leu His Phe
95 100 105

cca cta aga cct tac tat gta gga cct att agg ata tta aaa ccc cca 449
Pro Leu Arg Pro Tyr Tyr Val Gly Pro Ile Arg Ile Leu Lys Pro Pro
110 115 120

ttt cct cct att cct ttt ttt ctt gct att tac ctt cct atc tct aac 497
Phe Pro Pro Ile Pro Phe Phe Leu Ala Ile Tyr Leu Pro Ile Ser Asn
125 130 135

cct gag ccc caa ata aac atc acc acc gca gat aca aca atc acc aca 545
Pro Glu Pro Gln Ile Asn Ile Thr Thr Ala Asp Thr Thr Ile Thr Thr
140 145 150 155

aat ccc ccc acc act gca aca gca acc acc agg cac ttc cac aaa acc 593
Asn Pro Pro Thr Thr Ala Thr Ala Thr Thr Arg His Phe His Lys Thr
160 165 170

cac aat gac gat cag ctc ctc aac agt acc tat ctc ttc aac acc aga 641
His Asn Asp Asp Gln Leu Leu Asn Ser Thr Tyr Leu Phe Asn Thr Arg
175 180 185

gcc tgc cac ctc cat atc agc agc aac ccc cgc agc atc tac tga 686
Ala Cys His Leu His Ile Ser Ser Asn Pro Arg Ser Ile Tyr
190 195 200

aaatactact caaatctctg ccaaccgtcc tcacacagta ttgctcaatg ccactgtcca 746

agttacgact tccaaccaaa ctatattaag cagcccagcc tttaaaagtt tttggcaaaa 806

actctttgcc atttttgggt gaacatgcaa taaatgatat tttccaaact gctctgatat 866

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Met Lys Leu Thr Phe Phe Leu Gly Leu Leu Ala Leu Ile Ser Cys Phe
1 5 10 15

Thr Pro Ser Glu Ser Gln Arg Phe Ser Arg Arg Pro Tyr Leu Pro Gly
20 25 30

Gln Leu Pro Pro Pro Pro Leu Tyr Arg Pro Arg Trp Val Pro Pro Ser
35 40 45

Pro Pro Pro Pro Tyr Asp Ser Arg Leu Asn Ser Pro Leu Ser Leu Pro
50 55 60

Phe Val Pro Gly Arg Val Pro Pro Ser Ser Phe Ser Arg Phe Ser Gln
65 70 75 80

Ala Val Ile Leu Ser Gln Leu Phe Pro Leu Glu Ser Ile Arg Gln Pro
85 90 95

Arg Leu Phe Pro Gly Tyr Pro Asn Leu His Phe Pro Leu Arg Pro Tyr
100 105 110

Tyr Val Gly Pro Ile Arg Ile Leu Lys Pro Pro Phe Pro Pro Ile Pro
115 120 125

Phe Phe Leu Ala Ile Tyr Leu Pro Ile Ser Asn Pro Glu Pro Gln Ile
130 135 140

Asn Ile Thr Thr Ala Asp Thr Thr Ile Thr Thr Asn Pro Pro Thr Thr
145 150 155 160

Ala Thr Ala Thr Thr Arg His Phe His Lys Thr His Asn Asp Asp Gln
165 170 175

Leu Leu Asn Ser Thr Tyr Leu Phe Asn Thr Arg Ala Cys His Leu His
180 185 190

Ile Ser Ser Asn Pro Arg Ser Ile Tyr
195 200

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1 5

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Tyr Gln Arg Phe Ser Arg
1 5

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Cys Gln Arg Phe Ser Arg
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<223> Xaa2 is Gln or Glp when Xaa1 is not present.

Xaa2 is Gln when Xaa1 is Tyr or Cys.

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Xaa Xaa Arg Phe Ser Arg
1 5

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<220>
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<223> Xaa1 is Glp.

<400> 7

Xaa Arg Phe Ser Arg

1 5

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<211> 5
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<213> Rattus rattus

<400> 8

Gln His Asn Pro Arg
1 5

<210> 9
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<400> 9

Gln His Asn Pro
1

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<211> 5
<212> PRT
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Gln Arg Gly Pro Arg
1 5

<210> 11
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<400> 11

Gln Arg Gly Pro Arg Gly Pro
1 5

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<223> Synthetic Construct

<220>

<221> MISC_FEATURE
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<223> Arg at position 1 is modified with (7-methoxycoumarin-4-yl)acetyl

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<222> (10)..(10)
<223> hydroxy substituted 2,4-dinitrophenyl amino acid

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Arg Pro Pro Gly Phe Ser Ala Phe Lys Xaa
1 5 10

<210> 13
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<212> PRT
<213> Artificial Sequence

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<223> Synthetic Construct

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Ala at position 1 is modified with succinyl

<220>
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<222> (3)..(3)
<223> Phe at position 3 is modified with 7-amino-4-methyl coumarin

<400> 13

Ala Ala Phe
1

<210> 14
<211> 11
<212> PRT
<213> Homo sapiens

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Arg Phe Lys Phe Gln Gln Phe Phe Gly Leu Met
1 5 10

<210> 15
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<400> 15

Tyr	Gly	Gly	Phe	Met
1				5